

Figure 1: DNA and protein sequence of *A. calcoaceticus* s-GDH  
(without signalpeptide)

5           1 GATGTTCCCTCTAACTCCATCTCAATTGCTAAAGCGAAATCAGAGAACCTT 50  
      |||||||  
      1 AspValProLeuThrProSerGlnPheAlaLysAlaLysSerGluAsnPh 17

10          51 TGACAAGAAAGTTATTCTATCTAATCTAAATAAGCCGCACCGCGTTGTAT 100  
      |||||||  
      18 eAspLysLysValIleLeuSerAsnLeuAsnLysProHisAlaLeuLeuT 34

15          101 GGGGACCAGATAATCAAATTGGTTAACTGAGCGAGCAACAGGTAAAGATT 150  
      |||||||  
      35 rpGlyProAspAsnGlnIleTrpLeuThrGluArgAlaThrGlyLysIle 50

20          151 CTAAGAGTTAACATCCAGAGTCGGGTAGTGAAAAACAGTTTTTCAGGTAC 200  
      |||||||  
      51 LeuArgValAsnProGluSerGlySerValLysThrValPheGlnValPr 67

25          201 AGAGATTGTCAATGATGCTGATGGCAGAATGGTTATTAGGTTTGCCT 250  
      |||||||  
      68 oGluIleValAsnAspAlaAspGlyGlnAsnGlyLeuLeuGlyPheAlaP 84

30          251 TCCATCCTGATTAAAATAATCCTTATATCTATATTTCAGGTACATT 300  
      |||||||  
      85 heHisProAspPheLysAsnAsnProTyrIleTyrIleSerGlyThrPhe 100

35          301 AAAAATCCGAAATCTACAGATAAAGAATTACCGAACCAAACGATTATCG 350  
      |||||||  
      101 LysAsnProLysSerThrAspLysGluLeuProAsnGlnThrIleIleAr 117

40          351 TCGTTATACCTATAATAACAGATAACGCTCGAGAAGCCAGTCGATT 400  
      |||||||  
      118 gArgTyrThrTyrAsnLysSerThrAspThrLeuGluLysProValAspL 134

45          401 TATTAGCAGGATTACCTTCATCAAAAGACCATCAGTCAGGTGCTTGTC 450  
      |||||||  
      135 euLeuAlaGlyLeuProSerSerLysAspHisGlnSerGlyArgLeuVal 150

50          451 ATTGGGCCAGATCAAAAGATTATTACGATTGGTACCAAGGGCGTAA 500  
      |||||||  
      151 IleGlyProAspGlnLysIleTyrTyrThrIleGlyAspGlnGlyArgAs 167

55          501 CCAGCTTGCTTATTGTTCTGCCAATCAAGCACACATCGCCAACCTC 550  
      |||||||  
      168 nGlnLeuAlaTyrLeuPheLeuProAsnGlnAlaGlnHisThrProThrG 184

60          551 AACAAAGAACTGAATGGTAAAGACTATCACACCTATATGGGTAAAGTACTA 600  
      |||||||  
      185 lnGlnGluLeuAsnGlyLysAspTyrHisThrTyrMetGlyLysValLeu 200

65          601 CGCTTAAATCTGATGGAAGTATTCCAAAGGATAATCCAAGTTAACGG 650  
      |||||||  
      201 ArgLeuAsnLeuAspGlySerIleProLysAspAsnProSerPheAsnG1 217

70          651 GGTGGTTAGCCATATTACACTTGGACATCGTAATCCGCAGGGCTTAG 700  
      |||||||  
      218 yValValSerHisIleTyrThrLeuGlyHisArgAsnProGlnGlyLeuA 234

75          701 CATTCACTCCAAATGGTAAATTATTGCAGTCTGAACAAAGGCCAAACTCT 750  
      |||||||  
      235 laPheThrProAsnGlyLysLeuLeuGlnSerGluGlnGlyProAsnSer 250

Figure 1: Continued (second and last page)

751 GACGATGAAATTAAACCTCATTGTCAAAGTGGCAATTATGGTTGGCCGAA 800  
5 |||||  
251 AspAspGluIleAsnLeuIleValLysGlyGlyAsnTyrGlyTrpProAs 267  
  
801 TGTAGCAGGTTATAAAGATGATAGTGGCTATGCTTATGCAAATTATTCAG 850  
10 |||||  
268 nValAlaGlyTyrLysAspAspSerGlyTyrAlaTyrAlaAsnTyrSerA 284  
  
851 CAGCAGCCAATAAGTCATAAGGATTAGCTAAAATGGAGTAAAAGTA 900  
15 |||||  
285 laAlaAlaAsnLysSerIleLysAspLeuAlaGlnAsnGlyValLysVal 300  
  
901 GCCGCAGGGTCCCTGTGACGAAAGAATCTGAATGGACTGGTAAAAACTT 950  
20 |||||  
301 AlaAlaGlyValProValThrLysGluSerGluTrpThrGlyLysAsnPh 317  
  
951 TGTCCCACCATTAAAAACTTTATACCGTTCAAGATACTACAACATA 1000  
25 |||||  
318 eValProProLeuLysThrLeuTyrThrValGlnAspThrTyrAsnTyrA 334  
  
1001 ACGATCCAACCTGTGGAGAGATGACCTACATTGCTGGCAACAGTTGCA 1050  
30 |||||  
335 snAspProThrCysGlyGluMetThrTyrIleCysTrpProThrValAla 350  
  
1051 CCGTCATCTGCCTATGTCTATAAGGGCGTAAAAAGCAATTACTGGTG 1100  
35 |||||  
351 ProSerSerAlaTyrValTyrLysGlyGlyLysAlaIleThrGlyTr 367  
  
1101 GGAAAATACATTATTGGTTCATCTTAAACGTGGTGTCAATTTCGTA 1150  
40 |||||  
368 pGluAsnThrLeuLeuValProSerLeuLysArgGlyValIlePheArgI 384  
  
1151 TTAAGTTAGATCCAACCTATAGCACTACTTATGATGACGCTGTACCGATG 1200  
45 |||||  
385 leLysLeuAspProThrTyrSerThrThrTyrAspAspAlaValProMet 400  
  
1201 TTTAAGAGCAACAACCGTTATCGTGATGTGATTGCAAGTCCAGATGGAA 1250  
50 |||||  
401 PheLysSerAsnAsnArgTyrArgAspValIleAlaSerProAspGlyAs 417  
  
1251 TGTCTTATATGTATTAACACTGATACTGCCGGAAATGTCCAAAAGATGATG 1300  
45 |||||  
418 nValLeuTyrValLeuThrAspThrAlaGlyAsnValGlnLysAspAspG 434  
  
1301 GCTCAGTAACAAATACATTAGAAAACCCAGGATCTCTCATTAAGTTCAAC 1350  
50 |||||  
435 lySerValThrAsnThrLeuGluAsnProGlySerLeuIleLysPheThr 450  
  
1351 TATAAGGCTAAG 1362  
45 |||||  
451 TyrLysAlaLys 454

Figure 2: Amino acid sequences of *A. calcoaceticus* (top) and *A. baumannii* (bottom)

5        1 DVPLTPSQFAKAKSENFDKKVILSNLNKPHELLWGPDNQIWLTERATGKI 50  
      | : | | . | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      1 DIPLTTPAQFAKAKTENFDKKVILSNLNKPHELLWGPDNQIWLTERATGKI 50

10      51 LRVNPESGSVKTVFQVPEIVNDADGQNGLLGFAFHPDFKNNPYIYISGTF 100  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      51 LRVNPVSGSAKTVFQVPEIVSDADGQNGLLGFAFHPDFKHNPYIYISGTF 100

15      101 KNPKSTDKELPNQTIIIRRRTYNKSTDTEKPV DLLAGLPSSKDHQSGRLV 150  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      101 KNPKSTDKELPNQTIIIRRRTYNKTTDTFEKPIDLIAGLPSSKDHQSGRLV 150

20      151 IGPDQK IYYTIGDQGRNQLAYLFLPNQAQHTPTQQELNGKDYHTYMGKVL 200  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      151 IGPDQK IYYTIGDQGRNQLAYLFLSNQAQHTPTQQELNSKDYHTYMGKVL 200

25      201 RLNL DGSIPKDNPSFNGVVSHIYTLGHHRNPQGLAFTPNGKLLQSEQGPNS 250  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      201 RLNL DGSIPKDNPSFNGVVSHIYTLGHHRNPQGLAFAPNGKLLQSEQGPNS 250

30      251 DDEINLIVKG GNYGWP NVAGYKDDSGYAYAN YSAAANKS.IKDLAQNGVK 299  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      251 DDEINLVLKG GNYGWP NVAGYKDDSGYAYAN YSAAATNKSQIKDLAQNGIK 300

35      300 VAAGVPVTKESEWTGKNFV PPLK TLYTVQDT NYNDPTCGEMTYICWPTV 349  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      301 VATGVPVTKESEWTGKNFV PPLK TLYTVQDT NYNDPTCGEMAYICWPTV 350

40      350 APSSAYVYKG KKAI TG WENT LLVPSL KRG VIFRI KLDPTY STTYDDAVP 399  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      351 APSSAYVYTGGKAI PG WENT LLVPSL KRG VIFRI KLDPTY STT LDDAIP 400

45      400 MFKSNNRYRDVIA SPDG NVLYV LTD TAGNV QKDDG SVNT LENPGSLIKF 449  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
      401 MFKSNNRYRDVIA SP EGNT LYV LTD TAGNV QKDDG SVTH LENPGSLIKF 450

50      450 TYKAK 454  
      | | |  
      451 T YNGK 455

Figure 3: Schematic diagram of the plasmide with gene for s-GDH

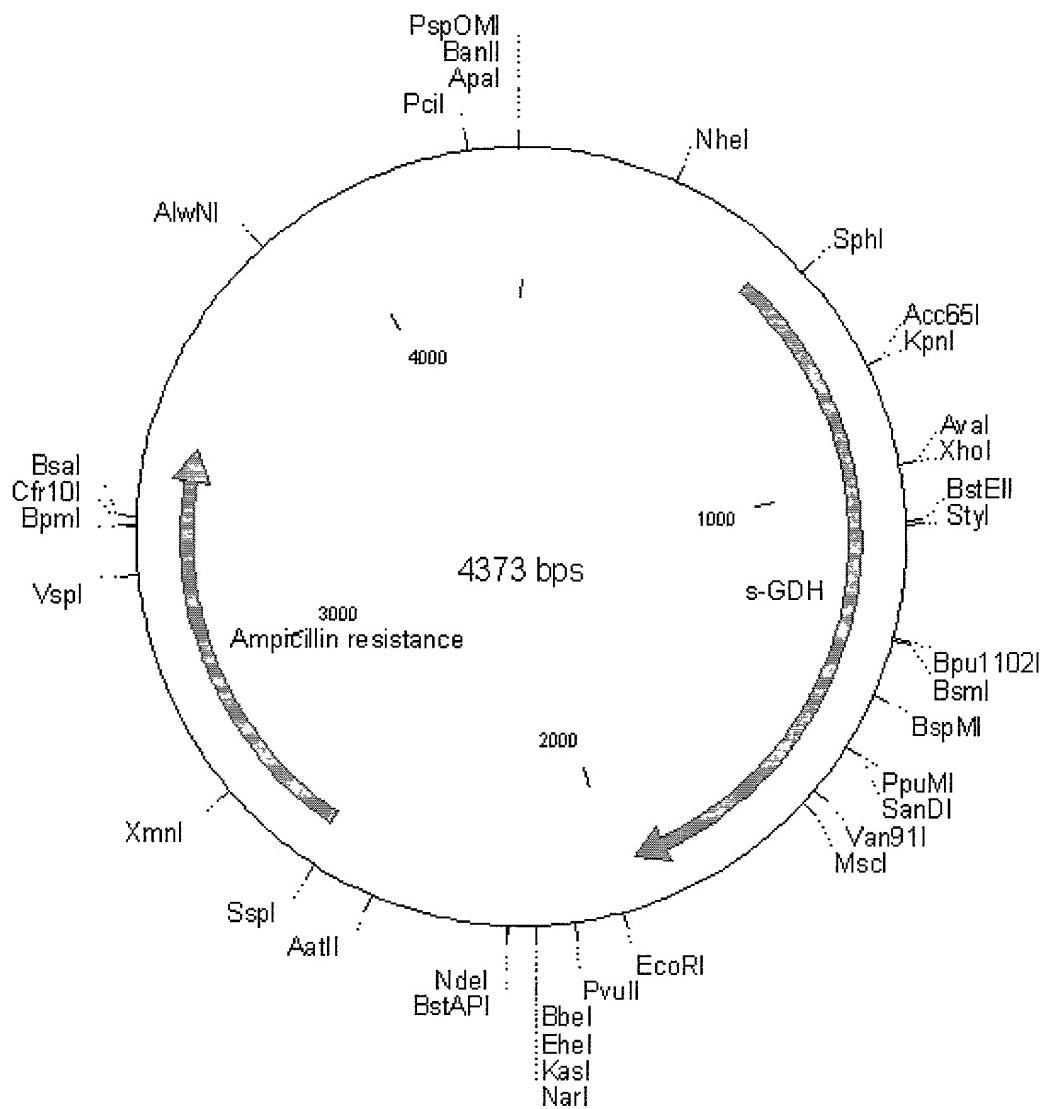


Figure 4: Nucleotide (DNA) sequence of the pACSGDH vector

1 CACTAACTGA TTACGCACCG CATGTAACCG TTTTCAATCT GTGAGTAAAT  
5 51 TCACAGTTA TTAACATTGT GATAGCTATG ATGACAACGT TTGTCGCACT  
10 101 GTAACTAACG TGTAACAGTT AGTTGTCAGT TTTGCTGGGG TATTCGCTT  
15 151 ATAAAAACCG TTATCACAAT ATCCCGCAC TACCGGACAA AAATAAAGAG  
20 201 TTGAATAAGA GCTTATCCA TTAGGGCTAT TTTACTTGCC ATTTTGGACC  
25 251 TGGGCAGTGC TCGCCAAAAC GCGTTAGCGT TTTGAACGCG CTAGCGCGG  
30 301 CCCGAAGGGC GAGCGTAGCG AGTCAAACCT CACGTACTAC GTGTACGCTC  
35 351 CGGTTTTTGC GCGCTGTCCG TGTCCAAACT GCTGCGCAA TAACGCCCTGG  
40 401 TGGGATAGGC TCTAAATACG CTTCGCGTT CAGTAACACG CGTTAACGTG  
45 451 CTGAACAGCC GGGCATTTTT TTACGCTATA CCCTACATAA TAAAACCGGA  
50 501 GCTACCATGA ATAAGAAGGT ACTGACCCCTT TCTGCCGTGA TGGCAAGTCT  
55 551 GTTATTCGGC GCGCACGCGC ATGCCGCCGA TGTTCCCTCTA ACTCCATCTC  
60 601 AATTGCTAA AGCGAAATCA GAGAACTTTG ACAAGAAAGT TATTCTATCT  
65 651 AATCTAAATA AGCCGCACGC GTGTTATGG GGACCGAGATA ATCAAATTG  
70 701 GTTAACTGAG CGAGCAACAG GTAAGATTCT AAGAGTTAAT CCAGAGTCGG  
75 751 GTAGTGTAAA AACAGTTTTT CAGGTACCAAG AGATTGTCAA TGATGCTGAT  
80 801 GGGCAGAATG GTTTATTAGG TTTTGCCTTC CATCCTGATT TTAAAAATAA  
85 851 TCCTTATATC TATATTCAG GTACATTAA AAATCCGAAA TCTACAGATA  
90 901 AAGAATTACC GAACCAAACG ATTATTCGTC GTTATACCTA TAATAAATCA  
95 951 ACAGATACGC TCGAGAAGCC AGTCGATTTA TTAGCAGGAT TACCTTCATC  
100 1001 AAAAGACCAT CAGTCAGGTC GTCTTGTCA TGGGCCAGAT CAAAAGATTT  
105 1051 ATTATACGAT TGGTGACCAA GGGCGTAACC AGCTTGCTTA TTTGTTCTTG  
110 1101 CCAAATCAAG CACAACATAC GCCAACTCAA CAAGAACTGA ATGGTAAAGA  
115 1151 CTATCACACC TATATGGGT AAGTACTACG CTTAAATCTT GATGGAAGTA  
120 1201 TTCCAAAGGA TAATCCAAGT TTTAACGGGG TGTTAGCCA TATTTATACA  
125 1251 CTTGGACATC GTAATCCGCA GGGCTTAGCA TTCACTCCAA ATGGTAAATT  
130 1301 ATTGCAGTCT GAACAAGGCC CAAACTCTGA CGATGAAATT AACCTCATTG  
135 1351 TCAAAGGTGG CAATTATGGT TGGCCGAATG TAGCAGGTTA TAAAGATGAT  
140 1401 AGTGGCTATG CTTATGCCAA TTATTCAAGCA GCAGCCAATA AGTCAATTAA  
145 1451 GGATTTAGCT CAAAATGGAG TAAAAGTAGC CGCAGGGGTC CCTGTGACGA  
150 1501 AAGAATCTGA ATGGACTGGT AAAAACTTG TCCCACCATT AAAAACTTA

Figure 4: Continued (second out of three pages)

1551 TATACCGTTC AAGATAACCA CAACTATAAC GATCCAAC TT GTGGAGAGAT  
5 1601 GACCTACATT TGCTGGCCAA CAGTTGCACC GTCATCTGCC TATGTCTATA  
1651 AGGGCGGTAA AAAAGCAATT ACTGGTTGGG AAAATACATT ATTGGTTCCA  
10 1701 TCTTTAAAAC GTGGTGTCA TTTCCGTATT AAGTTAGATC CAACTTATAG  
1751 CACTACTTAT GATGACGCTG TACCGATGTT TAAGAGCAAC AACCGTTATC  
1801 GTGATGTGAT TGCAAGTCCA GATGGGAATG TCTTATATGT ATTAACGTAT  
15 1851 ACTGCCGGAA ATGTCCAAA AGATGATGGC TCAGTAACAA ATACATTAGA  
1901 AAACCCAGGA TCTCTCATTA AGTTCACCTA TAAGGCTAAG TAATACAGTC  
20 1951 GCATTAAAAA ACCGATCTAT AAAGATCGGT TTTTTTAGTT TTAGAAAAGA  
2001 ATTCACTGGC CGTCGTTTA CAACGTCGTG ACTGGGAAAA CCCTGGCGTT  
2051 ACCCAACTTA ATCGCCTTGC AGCACATCCC CCTTCGCCA GCTGGCGTAA  
25 2101 TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGTTG CGCAGCCTGA  
2151 ATGGCGAATG GCGCCTGATG CCGTATTTTC TCCTTACGCA TCTGTGCGGT  
30 2201 ATTCACACCC GCATATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC  
2251 ATAGTTAACGC CAGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC  
2301 GGGCTTGTCT GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC  
35 2351 GGGAGCTGCA TGTGTCAGAG GTTTTCACCG TCATCACCGA AACGCGCGAG  
2401 ACGAAAGGGC CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA  
40 2451 TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA  
2501 ACCCCTATTT GTTTATTTTT CCAAATACAT TCAAATATGT ATCCGCTCAT  
2551 GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA  
45 2601 TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTG TGCGGCATT  
2651 TGCCTTCCTG TTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC  
50 2701 TGAAGATCAG TTGGGTGCAC GAGTGGTTA CATCGAACTG GATCTCAACA  
2751 GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG  
2801 AGCACTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC  
55 2851 CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG  
2901 TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA  
2951 AGAGAATTAT GCAGTGCTGC CATAACCAG AGTGATAACA CTGCGGCCAA  
60 3001 CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACCC GCTTTTTGC  
3051 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG

Figure 4: Continued (third and last page)

3101 AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT  
5 3151 GGCACAAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT  
3201 CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA  
10 3251 CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG  
3301 AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAAGCACTG GGGCCAGATG  
3351 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT  
15 3401 ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA  
3451 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT  
20 3501 TAAAACTTCA TTTTTAATT AAAAGGATCT AGGTGAAGAT CCTTTTGAT  
3551 AATCTCATGA CAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC  
3601 AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTCTGC  
25 3651 GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT  
3701 TGTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT  
3751 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG  
30 3801 GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
3851 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG  
35 3901 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA  
3951 CGGGGGGTTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA  
40 4001 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG  
4051 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC  
4101 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTA TAGTCCTGTC  
45 4151 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG  
4201 GGGCGGGAGC CTATGGAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC  
50 4251 TGGCCTTTG CTGGCCTTT GCTCACATGT TCTTTCTGC GTTATCCCCT  
4301 GATTCTGTGG ATAACCGTAT TACCGCCTT GAGTGAGCTG ATACCGCTCG  
4351 CCGCAGCCGA ACGACGGGGC CCG